

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 21:07:08 ; Search time 26 Seconds  
(without alignments)  
86.143 Million cell updates/sec

Title: US-09-659-737A-2

Sequence: 293 1 HRDIKAGNILLIKETIHHDDI.....EWHRTTKMSTAGTYAMNAP 54

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	239	81.6	394	1 M3K9_HUMAN	P80192 homo sapien
2	216	73.7	954	1 M3K9_HUMAN	Q02779 homo sapien
3	124.5	42.5	859	1 M3K9_HUMAN	Q12852 homo sapien
4	124.5	42.5	888	1 M3K9_MOUSE	Q06700 mus musculus
5	124.5	42.5	888	1 M3K9_RAT	Q03389 saccharomyc
6	108.5	37.0	1478	1 BCK1_YEAST	Q01389 schizosacch
7	101	34.5	589	1 SHK2_SCHPO	Q10056 schizosacch
8	100	34.1	328	1 KRAB_MOUSE	P28028 mus musculus
9	100	34.1	367	1 RML_AVT11	P10533 avian retic
10	100	34.1	450	1 RML_AVEVR	P27966 avian rous-
11	100	34.1	765	1 KRAB_HUMAN	P15056 homo sapien
12	100	34.1	806	1 RML_CHICK	Q04982 gallus gall
13	100	34.1	807	1 RML_COTJA	P34968 coturnia co
14	100	34.1	849	1 SRK6_BRAOL	Q09092 brassica ol
15	100	34.1	1080	1 NRK1_YEAST	P38692 saccharomyc
16	100	34.1	1116	1 NRK1_SCHPO	Q10407 schizosacch
17	99	33.8	488	1 KTI5_CAREL	P27636 saccharomyc
18	98.5	33.6	974	1 CCI5_YEAST	Q05609 arabidopsis
19	98	33.4	821	1 CTR1_ARATH	P43057 candida alb
20	98	33.4	1097	1 KPCI_CANAL	P05622 mus musculu
21	98	33.4	1098	1 PGDR_MOUSE	P20786 rattus norv
22	97	33.1	1088	1 PGDS_RAT	P16234 homo sapien
23	97	33.1	1089	1 PGDS_HUMAN	P26618 mus musculu
24	97	33.1	1089	1 PGDS_MOUSE	P08458 saccharomyc
25	96.5	32.9	490	1 SPK1_YEAST	P22216 saccharomyc
26	96.5	32.9	821	1 SPK1_YEAST	P22216 saccharomyc
27	96	32.8	1338	1 VGR1_CERPU	P17948 h vasculat
28	95.5	32.6	1307	1 PHYL_CERPU	P25848 ceratodon p
29	95	32.4	443	1 ST24_HUMAN	Q9Y660 homo sapien
30	95	32.4	506	1 MKK2_YEAST	P32491 saccharomyc
31	95	32.4	801	1 FGR3_MOUSE	Q61851 mus musculu
32	95	32.4	806	1 CKR2_CHICK	P18460 gallus gall
33	95	32.4	806	1 FGR3_HUMAN	P22607 homo sapien

34	95	32.4	812	1 FGR1_XENLA	P22182 xenopus lae
35	95	32.4	819	1 FGR1_CHICK	P21804 gallus gall
36	95	32.4	822	1 FGR1_HUMAN	P13562 mus sapien
37	95	32.4	822	1 FGR1_MOUSE	P16092 mus musculu
38	95	32.4	822	1 FGR1_RAT	Q04589 rattus norv
39	95	32.4	1087	1 PGDS_XENLA	P26619 xenopus lae
40	95	32.4	1106	1 PGDR_HUMAN	P09619 homo sapien
41	94	32.1	393	1 M3K7_DROME	P83104 drosophila
42	94	32.1	1333	1 VGR1_MOUSE	P35969 mus musculu
43	94	32.1	1336	1 VGR1_RAT	P53767 rattus norv
44	93	31.7	402	1 KROS_AVTISU	P00529 avian sarco
45	93	31.7	426	1 ST25_HUMAN	Q00506 homo sapien

## ALIGNMENTS

RESULT 1	M3K9_HUMAN	STANDARD:	PRT: 394 AA.
ID	M3K9_HUMAN		
AC	P80192:		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Mitogen-activated protein kinase kinase 9 (EC 2.7.1.-) (Mixed lineage kinase 1) (Fragment).		
DE	MAP3K9 OR MKK1 OR PRKEL.		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Colon epithelium;		
RX	MEDLINE=9338756; PubMed=8477742;		
RA	Dorow D.S., Devereux L., Dietzsch E., de Kretser T.,		
RT	*Identification of a new family of human epithelial protein kinases containing two leucine/isoleucine-zipper domains.*;		
RL	Eur. J. Biochem. 213:701-710(1993).		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF COLONIC, BREAST AND OESOPHAGEAL ORIGIN.		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	MAP KINASE KINASE SUBFAMILY.		
CC	PIR: S32467; S32467.		
DR	PIR: J00229; J00229.		
DR	HSSP: P12931; 1FMK.		
DR	Genev: HGNC:6861; MAP3K9.		
DR	MIM: 600136; .		
DR	InterPro: IPR000719; Euk_pkinase.		
DR	InterPro: IPR002290; Ser_thr_pkinase.		
DR	InterPro: IPR001245; Tyr_pkinase.		
DR	Pfam: PF00009; pkinase; 1.		
DR	Prodom: PD000001; Euk_pkinase; 1.		
DR	SMART: SM00219; TyrKc; 1.		
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.		
KW	Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase; ATP-binding.		
FT	NON_TER	1	
FT	DOMAIN	3	271
FT	NE_BIND	9	17
FT	ACT_SITE	127	127
FT	DOMAIN	289	310
FT	DOMAIN	324	345
FT	DOMAIN	354	368
SQ	SEQUENCE	394 AA;	44975 MW; DBA087D31047F8 CRC64;
Query Match	81.6%;	Score 239;	DB 1; Length 394;
Best Local Similarity	77.8%;	Pred. No. 3;	5e-22;
Matches	42;	Conservative	7; Mismatches 5; Indels 0; Gaps 0;

OY 1 HRDIFAGNILLLEKIEHDDICNKTITDFGLAREHRTTKMSAGTYAWMAPE 54  
 DB 125 HRDLKSSNILLLOKVENGDLSNKLITTDGLAREHRTTKMSAGTYAWMAPE 178

RESULT 2  
 M3KA\_HUMAN STANDARD; PRT; 954 AA.  
 ID M3KA\_HUMAN 002779; Q12761; Q14871;  
 AC 01-FEB-1994 (Rel. 28, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)  
 GN MAP3K10 OR MLK2 OR MST.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96128179; PubMed=8536694;  
 RA Dorew D.S., Deyereux L., Tu G.F., Price G., Nicholl J.K.,  
 RA Sutherland G.R., Simpson R.J.;  
 RT "complete nucleotide sequence, expression, and chromosomal  
 RT localisation of human mixed-lineage kinase 2.";  
 RL Eur. J. Biochem. 234:492-500(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=95249256; PubMed=7731697;  
 RA Kato M., Hirai M., Sugimura T., Terada M.;  
 RT "Cloning and characterization of MST, a novel (putative)  
 RT serine/threonine kinase with SH3 domain.";  
 RL Oncogene 10:1447-1451(1995).  
 RN [3]  
 RP SEQUENCE OF 244-480 FROM N.A.  
 RC TISSUE=Colon epithelium;  
 RX MEDLINE=93238756; PubMed=8477742;  
 RA Dorew D.S., Deyereux L., Dietzsch E., de Kretser T.;  
 RT "Identification of a new family of human epithelial protein kinases  
 RT containing two leucine/isoleucine-zipper domains.";  
 RL Eur. J. Biochem. 213:701-710(1993).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE KINASE SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL; X90846; CAA62351.1; -  
 CC EMBL; Z48615; CAA88531.1; -  
 CC PIR; S32468; S32468.  
 CC HSSP; P13362; 1FGK.  
 CC Genew; HGNC:6849; MAP3K10.  
 CC MIM; 600137; -  
 CC InterPro; IPR000719; Euk\_pkinase.  
 CC InterPro; IPR001452; SH3.  
 CC InterPro; IPR004040; STY\_pkinase.  
 CC InterPro; IPR002290; Ser\_thr\_pkinase.  
 CC InterPro; IPR001245; Tyr\_pkinase.  
 CC Pfam; PF000018; SH3\_1.  
 CC Pfam; PF000059; Pkinase\_1.  
 CC PRINTS; PR00452; SH3DOMAIN.  
 CC PRINTS; PR00109; TYRKINASE.

DR Prodom: PD000001; Euk\_Pkinase; 1.  
 DR Prodom: PD000066; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00221; STYK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KM Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;  
 FT ATP-binding; SH3 domain.  
 FT DOMAIN 2  
 FT DOMAIN 16  
 FT DOMAIN 98  
 FT NP\_BIND 104  
 FT BINDING 125  
 FT ACT\_SITE 222  
 FT DOMAIN 384  
 FT DOMAIN 419  
 FT DOMAIN 449  
 FT DOMAIN 463  
 FT CONFLICT 462  
 FT CONFLICT 465  
 FT CONFLICT 471  
 FT CONFLICT 807  
 FT CONFLICT 818  
 SQ SEQUENCE 954 AA; 103623 MW; 538P4AA55B0BADA CRC64;

Query Match 73.7%; Score 216; DB 1; Length 954;  
 Best Local Similarity 72.2%; Pred. No. 6.2e-19; Mismatches 7; Indels 0; Gaps 0;  
 Matches 39; Conservative 8;

OY 1 HRDIFAGNILLLEKIEHDDICNKTITDFGLAREHRTTKMSAGTYAWMAPE 54  
 DB 220 HRDLKSSNILLLOKVENGDLSNKLITTDGLAREHRTTKMSAGTYAWMAPE 273

RESULT 3  
 M3KC\_HUMAN STANDARD; PRT; 859 AA.  
 ID M3KC\_HUMAN 012852;  
 AC 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)  
 DE (leucine-zipper protein kinase) (ZPK).  
 GN MAP3K12 OR ZPK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Teraocarcinoma;  
 RX MEDLINE=94311945; PubMed=8037767;  
 RA Reddy U.R., Pleasure D.;  
 RT "Cloning of a novel putative protein kinase having a leucine zipper  
 RT domain from human brain.";  
 RL Biochem. Biophys. Res. Commun. 202:613-620(1994).  
 CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.  
 CC Phosphorylates beta-casein, histone 1 and myelin basic protein in  
 CC vitro.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By  
 CC similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in brain and kidney.  
 CC -1- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol  
 CC under basal conditions and dephosphorylated when membrane-  
 CC associated (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE KINASE SUBFAMILY.  
 CC -----  
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DR EMBL: U07358; AAA67343.1; -  
 DR HSSP: P12931; 1PMK.  
 DR Genew: HGNC:6851; MAP3K12.  
 DR MIM: 600447; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Magnesium; Membrane.  
 FT DOMAIN 125 366 PROTEIN KINASE.  
 FT NP\_BIND 131 139 APP (BY SIMILARITY).  
 FT BINDING 152 152 ATP (BY SIMILARITY).  
 FT ACT\_SITE 236 236 BY SIMILARITY.  
 FT DOMAIN 665 668 POLY-PRO.  
 FT DOMAIN 720 725 POLY-GLU.  
 SQ SEQUENCE 859 AA; 93188 MW; 0E5209792C5C6F05 CRC64;

Query Match 42.5%; Score 124.5; DB 1; Length 859;  
 Best Local Similarity 50.9%; Pred. No. 1.1e-07;  
 Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;

OY 1 HROIKAGNITLLEKIEHDDCNKTKITDGLAREW-HRTTKMSTAGTYAMAP 54  
 Db 234 HRDLKSPNML-----ITYDDV-----VKISDGTGSKELSDKSTKSPAGTYAMAP 280

RESULT 4  
 M3KC\_MOUSE STANDARD; PRT; 888 AA.  
 AC 060700; P70286;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mitogen-activated protein kinase kinase 12 (EC 2.7.1.37)  
 DE (leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing  
 DE kinase) (DLK).  
 CN MAP3K12 OR ZPK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=Brain;  
 RX MEDLINE=95074107; PubMed=983011;  
 RA Holzman L.B., Merritt S.E., Fan G.;  
 RT "Identification, molecular cloning, and characterization of dual  
 RT leucine zipper bearing kinase. A novel serine/threonine protein kinase  
 RT that defines a second subfamily of mixed lineage kinases.";  
 RU J. Biol. Chem. 269:30808-30817(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ICR X Swiss Webster; TISSUE=Brain;  
 RX MEDLINE=96365388; PubMed=8769565;  
 RA Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;  
 RT "Cell-specific expression of the zpk gene in adult mouse tissues.";  
 RU DNA Cell Biol. 15:631-642(1996).  
 RN [3]  
 RP PHOSPHORYLATION, AND MUTAGENESIS OF LYS-185 AND GLU-192.  
 RX MEDLINE=96279269; PubMed=8663324;

RA Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;  
 RT "Characterization of dual leucine zipper-bearing kinase, a mixed  
 RT lineage kinase present in synaptic terminals whose phosphorylation  
 RT state is regulated by membrane depolarization via calcineurin.";  
 RL J. Biol. Chem. 271:16888-16896(1996).  
 CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.  
 CC phosphorylates beta-casein, histone 1 and myelin basic protein in  
 CC vitro.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
 CC -1- COFACTOR: Magnesium.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated.  
 CC -1- TISSUE SPECIFICITY: Expressed in brain, kidney, lung, heart,  
 CC testis, gastrointestinal tract, stomach, liver and pancreas.  
 CC Within the nervous system, predominantly expressed in neurons and  
 CC enriched in synaptic terminals.  
 CC -1- PFM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol  
 CC under basal conditions and dephosphorylated when membrane-  
 CC associated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE SUBFAMILY.

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DR EMBL: U14636; AAA57280.1; -  
 DR EMBL: U23789; AAB17123.1; -  
 DR HSSP: P12931; 1PMK.  
 DR MGD: MGI:1346881; Map3K12.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Magnesium; Membrane.  
 FT DOMAIN 158 399 PROTEIN KINASE.  
 FT NP\_BIND 164 172 ATP (BY SIMILARITY).  
 FT BINDING 185 185 BY SIMILARITY.  
 FT ACT\_SITE 269 269 POLY-GLY.  
 FT DOMAIN 36 62 POLY-PRO.  
 FT DOMAIN 668 671 POLY-PRO.  
 FT DOMAIN 753 758 POLY-GLU.  
 FT MUTAGEN 185 185 K->A: NO CATALYTIC ACTIVITY.  
 FT MUTAGEN 192 192 E->A: NO CHANGE.  
 FT MUTAGEN 192 192 V->A (IN REF. 2).  
 FT CONFLICT 16 18 KL->NV (IN REF. 2).  
 FT CONFLICT 28 29 S->T (IN REF. 2).  
 FT CONFLICT 382 382 EQ->D (IN REF. 2).  
 FT CONFLICT 494 495 N->D (IN REF. 2).  
 FT CONFLICT 517 517 E->G (IN REF. 2).  
 FT CONFLICT 794 794  
 SQ SEQUENCE 888 AA; 96083 MW; CFECFD134F889ABB CRC64;

Query Match 42.5%; Score 124.5; DB 1; Length 888;  
 Best Local Similarity 50.9%; Pred. No. 1.2e-07;  
 Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;

OY 1 HROIKAGNITLLEKIEHDDCNKTKITDGLAREW-HRTTKMSTAGTYAMAP 54  
 Db 267 HRDLKSPNML-----ITYDDV-----VKISDGTGSKELSDKSTKSPAGTYAMAP 313

RESULT 5  
 M3KC\_RAT

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ID M3KC_RAT STANDARD: PRT: 888 AA.
AC 063796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE M10gen-activated protein kinase kinase 12 (EC 2.7.1.37)
DE (MAPK-upstream kinase) (MUK).
GN MAP3K12 OR MUK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96226099; PubMed=8637721;
RA Hirai S., Itawa M., Osada S., Spyrou G., Ohno S.;
RT "Activation of the JNK pathway by distantly related protein kinases,
RT MEKK and MUK."
RL Oncogene 12:641-650(1996).
CC -1- FUNCTION: May be an activator of the JNK/SAPK pathway.
CC Phosphorylates beta-casein, histone H and myelin basic protein in
CC vitro.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- COFACTOR: Magnesium.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
CC similarity).
CC -1- PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol
CC under basal conditions and dephosphorylated when membrane-
CC associated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: DA9785; BAA08621.1; -
DR HSSP: P12931; 1FMK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00221; STYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Magnesium; Membrane.
FT DOMAIN 158 399 PROTEIN KINASE.
FT NP_BIND 164 172 ATP (BY SIMILARITY).
FT BINDING 185 185 ATP (BY SIMILARITY).
FT ACT_SITE 269 269 ATP (BY SIMILARITY).
FT DOMAIN 56 62 POLY-GLY.
FT DOMAIN 668 671 POLY-PRO.
FT DOMAIN 698 701 POLY-PRO.
FT DOMAIN 753 758 POLY-GLU.
SQ SEQUENCE 888 AA; 96307 MW; 52AD964006BAE149 CRC64;

Query Match 42.5%; Score 124.5; DB 1; Length 888;
Best Local Similarity 50.9%; Pred. No. 1.2e-07;
Matches 28; Conservative 11; Mismatches 7; Indels 9; Gaps 3;

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QY 1 HRDIKAGNILLERIKEDICNKTITDGLAREW-HRTTKSTAGTAYAMAP 54
Db 267 HRDUKSPNML-----ITVDV-----VKISDGTSEKLSKSTKSPAGTAYAMAP 313
RESULT 6

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ID BCK1_YEAST STANDARD: PRT: 1478 AA.
AC 001389; P32894;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein kinase BCK1/SLK1/SSP31 (EC 2.7.-.-).
GN BCK1 OR SLK1 OR SSP31 OR IAS3 OR YJ1095W OR J0906.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92186847; PubMed=1545797;
RA Costigan C., Gehring S., Snyder M.;
RT "A synthetic lethal screen identifies SLK1, a novel protein kinase
RT homolog implicated in yeast cell morphogenesis and cell growth."
RL Mol. Cell. Biol. 12:1162-1178(1992).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=92104496; PubMed=1840547;
RA Irie K., Ataki H., Oshima Y.;
RT "A new protein kinase, SSP31, modulating the SWP3 gene-product
RT involved in plasmid maintenance in Saccharomyces cerevisiae."
RL Gene 108:139-144(1991).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=EG123;
RX MEDLINE=92107166; PubMed=1729597;
RA Lee K.S., Levin D.E.;
RT "Dominant mutations in a gene encoding a putative protein kinase
RT (BCK1) bypass the requirement for a Saccharomyces cerevisiae protein
RT kinase C homolog."
RL Mol. Cell. Biol. 12:172-182(1992).
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95176706; PubMed=7871887;
RA Miesha T., Boles E., Schaaff-Gerstenschlaeger I., Schmitt S.,
RA Zimmermann F.K.;
RT "Sequence and function analysis of a 9.74 kb fragment of
RT Saccharomyces cerevisiae chromosome X including the BCK1 gene."
RL Yeast 10:1481-1488(1994).
RN (5)
RP SEQUENCE OF 602-1104 FROM N.A.
RA Cusick M.E.;
RT Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN A SIGNAL
CC TRANSDUCTION PATHWAY THAT PLAY A ROLE IN YEAST CELL MORPHOGENESIS
CC AND CELL GROWTH. THIS PATHWAY SEEMS TO STARTS BY SWP3; THEN
CC INVOLVE THE KINASE PKC1 THAT MAY ACT ON THIS KINASE. BCK1 PROBABLY
CC PHOSPHORYLATES MKK1 AND MKK2 WHICH THEMSELVES PHOSPHORYLATE THE
CC MPK1 KINASE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE KINASE KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: M84389; -; NOT_ANNOTATED_CDS.
DR EMBL: D10389; BAA01226.1; -
DR EMBL: X60227; CAA42788.1; -
DR EMBL: X77923; CAA54896.1; -
DR EMBL: Z49370; CAA89389.1; -
DR EMBL: Z49369; CAA89388.1; -
DR EMBL: M88604; AAA21179.1; -

```



Best Local Similarity 51.8%; Pred. No. 6e-05;  
Matches 29; Conservative 5; Mismatches 12; Indels 10; Gaps 4;

QY 1 HRDIKAGNILLLEKIEHDDICKTKITDFFGL-AREHRTTKMST-AGTYAMAAPE 54  
DB 432 HRDIKSDNVL-----DMSGN-IKITDFGFCARLSNRINKRYTWGCTPYMAPE 479

## RESULT 8

KRAB\_MOUSE STANDARD; PRT; 328 AA.  
AC P28028;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE B-RAF proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)  
DE (fragment).  
GN BRAF OR B-RAF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;

RP SEQUENCE FROM N.A.  
RX MEDLINE=91271351; PubMed=2052597;  
RA Miki T., Fleming T.P., Crescenzi M., Molloy C.J., Blam S.B.,  
RA Reynolds S.H., Aaronson S.A.;  
RT "Development of a highly efficient expression cDNA cloning system:  
RT Application to oncogene isolation."  
RL Proc. Natl. Acad. Sci. U.S.A. 88:5167-5171(1991).  
CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
CC FROM THE CELL MEMBRANE TO THE NUCLEUS.  
CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF  
CC HIPPOCAMPAL NEURON.  
CC -1- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES  
CC A T(11;22)(p11;p23) ONCOGENE ORIGINALLY ISOLATED FROM A FETAL  
CC INDUCED HEPATOMA.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -1- MIL/RAF SUBFAMILY.

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CC -----  
DR EMBL; M64429; AAA37320.1; ALT\_INIT.  
DR PIR; A40951; TVMSBF.  
DR HSSP; P08631; IAD5.  
DR MGD; MG1:88190; Braf.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR004040; STY\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00221; STYKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Transferrase; Serine/threonine-protein kinase; Proto-oncogene;  
KW ATP-binding; Chromosomal translocation.

FT DOMAIN 1 279  
FT NP\_BIND 25 33 PROTEIN KINASE.  
FT BINDING 45 45 ATP (BY SIMILARITY).  
FT ACT\_SITE 138 138 BY SIMILARITY.  
SQ SEQUENCE 328 AA; 36986 MW; 67A2EBF878A7BE3D CRC64;

Query Match 34.1%; Score 100; DB 1; Length 328;  
Best Local Similarity 43.3%; Pred. No. 4.3e-05;  
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDIKAGNILLLEKIEHDDICKTKITDFFGL-AREHRTTKMST-AGTYAMAAPE 54  
DB 136 HRDIKSNMIFL-----HEDL--TKVIGDFGLATYKSMSSGSHOPEOL--GSILMAAPE 185

## RESULT 9

RML\_AVII1 STANDARD; PRT; 367 AA.  
AC P10533; 085612; 085613; 085614;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine/threonine-protein kinase transforming protein Rml1  
DE (EC 2.7.1.37).  
GN V-RML.  
OS Avian retrovirus IC10.  
OC Viruses; Retroviridae; Retroviridae; Avian type C retroviruses.  
OX NCBI\_Taxid=11874;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89160254; PubMed=2537952;  
RA Eychene A., Marx M., Dezelic P., Calothy G.;  
RT "Complete nucleotide sequence of IC10, a retrovirus containing the  
RT Rml1 oncogene transduced in chicken neuroretina cells infected with  
RT avian retrovirus RAV-1."  
RL Nucleic Acids Res. 17:1250-1250(1989).

RP SEQUENCE FROM N.A.  
RX MEDLINE=89091077; PubMed=2850163;  
RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,  
RA Dezelic P., Pessac B., Calothy G.;  
RT "A novel oncogene related to c-mil is transduced in chicken  
RT neuroretina cells induced to proliferate by infection with an avian  
RT lymphomatosus virus."  
RL EMO J. 7:3369-3373(1988).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL  
CC POLYPEPTIDE.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC -1- MIL/RAF SUBFAMILY.

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CC -----  
DR EMBL; X13744; CAA32008.1; ALT\_SEQ.  
DR EMBL; X13438; CAA31790.1; ALT\_SEQ.  
DR PIR; S01645; TVEVMT.  
DR HSSP; P08631; IAD5.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR004040; STY\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00221; STYKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Polypeptin; Serine/threonine-protein kinase; Transferrase; Oncogene;  
KW ATP-binding.

FT DOMAIN 67 327  
FT NP\_BIND 73 81 PROTEIN KINASE.  
FT BINDING 93 93 ATP (BY SIMILARITY).  
FT ACT\_SITE 186 186 BY SIMILARITY.  
SQ SEQUENCE 367 AA; 41023 MW; E137ARCDBC8398A CRC64;

Query Match 34.1%; Score 100; DB 1; Length 367;  
Best Local Similarity 43.3%; Pred. No. 4.8e-05;

Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;  
 QY 1 HRDRIKGNILLEKIEHDICNKTITDEGLA---REM---HRTTKMSTAGTYAMMAPE 54  
 DB 184 HRDLKSNMIFL-----HEDL---TVKIGDFGLATYKSRMSSGSHQEQLS--GSILMAPE 233

## RESULT 10

RMLL\_AVEVR STANDARD: PRT: 450 AA.  
 ID RMLL\_AVEVR STANDARD: PRT: 450 AA.  
 AC P27966;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase transforming protein Rml1  
 DE (EC 2.7.1.37).  
 GN V-RML1.  
 OS Avian rous-associated virus type 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.  
 OX NCBI\_TaxID=11950;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91251215; PubMed=1645786;  
 RA Felder M.P., Eyche A., Barnier J.V., Calogeraki I., Calothy G.,  
 RA Marx M.,  
 RT "Common mechanism of retrovirus activation and transduction of c-mil  
 RT and c-Rml1 in chicken neuroretina cells infected with Rous-associated  
 RT virus type 1."  
 RL J. Virol. 65:3633-3640(1991).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV  
 CC POLYPROTEIN. BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MIL/RAF SUBFAMILY.

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DR EMBL: M62407; AAA42549.1; -  
 DR PIR: A40341; TVFVNR.  
 DR HSP: P08631; 1AD5.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00221; STYKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Polyprotein; Serine/threonine-protein kinase; Transferase; Oncogene;  
 KW ATP-binding.  
 FT DOMAIN 83 343 PROTEIN KINASE.  
 FT NP\_BIND 89 97 ATP (BY SIMILARITY).  
 FT BINDING 109 109 ATP (BY SIMILARITY).  
 FT ACT\_SITE 202 202 BY SIMILARITY.  
 SQ SEQUENCE 450 AA; 50313 MM; 6581AAAF2253CB622 CRC64;

Query Match 34.1%; Score 100; DB 1; Length 450;  
 Best Local Similarity 43.3%; Pred. No. 6e-05; Indels 16; Gaps 5;  
 Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDRIKGNILLEKIEHDICNKTITDEGLA---REM---HRTTKMSTAGTYAMMAPE 54  
 DB 200 HRDLKSNMIFL-----HEDL---TVKIGDFGLATYKSRMSSGSHQEQLS--GSILMAPE 249

RESULT 11

KRAB\_HUMAN STANDARD: PRT: 765 AA.  
 ID KRAB\_HUMAN STANDARD: PRT: 765 AA.

AC P15056;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1995 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE B-Raf proto-oncogene serine/threonine-protein kinase (EC 2.7.1.-)  
 DE (p94) (V-Raf murine sarcoma viral oncogene homolog B1).  
 GN BRAF OR BRAF1 OR KAPB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Testis;  
 RX MEDLINE=92375040; PubMed=1508179;  
 RA Stephens R.M., Sithanandam G., Copeland T.D., Kaplan D.R., Rapp U.R.,  
 RA Morrison D.K.;  
 RT "95-kilodalton B-Raf serine/threonine kinase: identification of the  
 RT protein and its major autophosphorylation site."  
 RL Mol. Cell. Biol. 12:3733-3742(1992).  
 RN [2]  
 RP SEQUENCE OF 116-765 FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=9113728; PubMed=2284096;  
 RA Sithanandam G., Kolch W., Duh F.-M., Rapp U.R.;  
 RT "Complete coding sequence of a human B-Raf cDNA and detection of  
 RT B-Raf protein kinase with isozyme specific antibodies."  
 RL Oncogene 5:1775-1780(1990).  
 RN [3]  
 RP SEQUENCE OF 438-765 FROM N.A.  
 RX MEDLINE=88302178; PubMed=3043188;  
 RA Ikawa S., Fukui M., Ueyama Y., Tamaoki N., Yamamoto T., Toyoshima K.;  
 RT "B-Raf, a new member of the raf family, is activated by DNA  
 RT rearrangement."  
 RL Mol. Cell. Biol. 8:2651-2654(1988).  
 CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS  
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.  
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF  
 CC HIPPOCAMPAL NEURON.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: CEREBRUM AND TESTES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHOSPHO-ESTER AND DAG  
 CC BINDING DOMAIN.

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DR EMBL: M95712; AAA35609.1; -  
 DR EMBL: M21001; AAA96495.1; -  
 DR PIR: A31850; TVHUBF.  
 DR PIR: S13798; S13798.  
 DR HSP: P04049; 1PAR.  
 DR Genew; HGNC:1097; BRAF.  
 DR MIM; 164757; -  
 DR InterPro: IPR002219; DAG\_PE\_bind.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003116; RBD.  
 DR InterPro: IPR004040; STY\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00130; DAG\_PE\_bind; 1.  
 DR Pfam: PF02196; RBD; 1.  
 DR PRINTS: PR00008; DAGPEDOMAIN.  
 DR ProDom: PD000001; Euk\_pkinase; 1.

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DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR SMART; SM00221; STYK; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
KW ATP-binding; Phorbol-ester binding; Phosphorylation.
FT DOMAIN 6 11 POLY-SER.
FT DOMAIN 121 128 POLY-SER.
FT DOMAIN 234 279 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 427 431 POLY-SER.
FT NP_BIND 456 476 PROTEIN KINASE.
FT BINDING 462 470 ATP (BY SIMILARITY).
FT BINDING 482 482 ATP (BY SIMILARITY).
FT ACT_SITE 575 575 BY SIMILARITY.
FT MOD_RES 372 372 PHOSPHORYLATION (AUTO-).
FT CONFLICT 765 765 H->D (IN REF. 3).
SQ SEQUENCE 765 AA; 84490 MW; 93A9EE4D6C1C68E CRC64;

Query Match 34.1%; Score 100; DB 1; Length 765;
Best Local Similarity 43.3%; Pred. No. 0.0001;
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDIAKGNILLLEKIEHDDICKTKITDFGLA---REW---HRTTKMSTAGTYAMWAP 54
DB 573 HRDIAKGNINFL-----HEDL---TVKIDGFLATVKSRSMSGSHOFEQLS--GSTIMWAP 622

RESULT 12
RMIL_CHICK STANDARD; PRT; 806 AA.
ID RMIL_CHICK
AC C04982;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).
GN C-MAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
ON NCBI_TaxID=9031;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes, and Fibroblast;
RA MEDLINE=93312327; PubMed=8323553;
RA Calogeraki I., Barnier J.V., Eychene A., Felder M.-P., Calothy G.,
RA Marx M.,
RT "Genomic organization and nucleotide sequence of the coding region of
RT the chicken c-Rml1(B-raf-1) proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 193:1324-1331(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC NEURAL CELLS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEURAL TISSUE.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC ML/RAE SUPFAMILY.
CC -1- SIMILARITY: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC BINDING DOMAIN.
CC -----
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CC -----
CC EMBL; X67052; CAA47436.1; -.
CC PIR; J0612; J0612.
CC HSSP; P04049; IFAF.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR00719; Euk_pkinase.
DR InterPro; IPR003116; RBD.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR pfam; PF00069; pkinase; 1.
DR pfam; PF00130; DAG_PE-bind; 1.
DR pfam; PF02196; RBD; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00455; RBD; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Proto-oncogene; Transferrase; Serine/threonine-protein kinase;
KW ATP-binding; Nuclear protein; Alternative splicing; Zinc;
KW Phorbol-ester binding; Phosphorylation.
FT DOMAIN 122 129 POLY-SER.
FT DOMAIN 235 280 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 248 260 CYS-RICH.
FT NP_BIND 497 511 PROTEIN KINASE.
FT BINDING 503 523 ATP (BY SIMILARITY).
FT BINDING 523 523 ATP (BY SIMILARITY).
FT ACT_SITE 616 616 BY SIMILARITY.
FT VARSPLIT 393 432 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 806 AA; 89365 MW; 8E3FAD5274FB75C CRC64;

Query Match 34.1%; Score 100; DB 1; Length 806;
Best Local Similarity 43.3%; Pred. No. 0.0001;
Matches 26; Conservative 9; Mismatches 9; Indels 16; Gaps 5;

QY 1 HRDIAKGNILLLEKIEHDDICKTKITDFGLA---REW---HRTTKMSTAGTYAMWAP 54
DB 614 HRDIAKGNINFL-----HEDL---TVKIDGFLATVKSRSMSGSHOFEQLS--GSTIMWAP 663

RESULT 13
RMIL_COTUJA STANDARD; PRT; 807 AA.
ID RMIL_COTUJA
AC P34908;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RMIL serine/threonine-protein kinase (EC 2.7.1.37).
GN C-MAIL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
ON NCBI_TaxID=93934;
RX [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92319540; PubMed=1620546;
RA Eychene A., Barnier J.V., Dezelic P., Marx M., Laugier D.,
RA Calogeraki I., Calothy G.,
RT "Quali neurorretina c-Rml1(B-raf) proto-oncogene cDNAs encode two
RT proteins of 93.5 and 95 kDa resulting from alternative splicing.";
RL Oncogene 7:1315-1323(1992).
CC -1- FUNCTION: MAY PLAY A ROLE IN TRANSDUCING SPECIFIC SIGNALS IN
CC NEURAL CELLS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

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